

## Supplementary Material

AMR-meta: a k-mer and metafeature approach to classify antimicrobial resistance from high-throughput short-read metagenomics data

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**Supplementary Figure S1 (next page).** Cumulative FP ratio over  $PSS_{cla}$  subsets. Negative short reads from the set genomes have been collated according to the growing similarity of BLAST matches, i.e., 70% to 75%, 75+% to 80%, 80+% to 85%, and 85+% to 90%. FP ratio has been calculated for each subset. The figure reports the cumulative FP ratio for the different thresholds. Sets not represented in the figure did not provide genomes with similarities within the corresponding column ranges.

Cumulative FP ratio

